



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/595,947D

DATE: 10/27/2003

TIME: 09:29:14

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\10272003\I595947D.raw

5 <110> APPLICANT: ICARD-LIEPKALNS, Christine
6 MALLET, Jacques
7 RAVASSARD, Philippe
9 <120> TITLE OF INVENTION: POLYPEPTIDES OF THE "BASIC-HELIX-LOOP-HELIX" bHLH
10 FAMILY, CORRESPONDING NUCLEIC ACID SEQUENCES ;
12 <130> FILE REFERENCE: P26,952 USA
14 <140> CURRENT APPLICATION NUMBER: US 09/595,947D
15 <141> CURRENT FILING DATE: 2000-06-16
17 <150> PRIOR APPLICATION NUMBER: FR96/15651
18 <151> PRIOR FILING DATE: 1996-12-19
20 <150> PRIOR APPLICATION NUMBER: PCT/FR97/02368
21 <151> PRIOR FILING DATE: 1997-12-19
23 <150> PRIOR APPLICATION NUMBER: US 09/331,356
24 <151> PRIOR FILING DATE: 1999-07-12
26 <160> NUMBER OF SEQ ID NOS: 40
28 <170> SOFTWARE: PatentIn Ver. 3.1

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ERRORED SEQUENCES

129 <210> SEQ ID NO: 5
130 <211> LENGTH: 18
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primers
137 <400> SEQUENCE: 5 cgcggtgtcc tgcccacc 18
E--> 137 5 cgcggtgtcc tgcccacc 18 *← move this under <400> 5 line*
164 <210> SEQ ID NO: 8
165 <211> LENGTH: 214
166 <212> TYPE: PRT
167 <213> ORGANISM: Rattus norvegicus *p.2*
169 <400> SEQUENCE: 8
170 Met Ala Pro His Pro Leu Asp Ala Pro Thr Ile Gln Val Ser Gln Glu
171 1 5 10 15
173 Thr Gln Gln Pro Phe Pro Gly Ala Ser Asp His Glu Val Leu Ser Ser
174 20 25 30
176 Asn Ser Thr Pro Pro Ser Pro Thr Leu Val Pro Arg Asp Cys Ser Glu
177 35 40 45
179 Ala Glu Ala Gly Asp Cys Arg Gly Thr Ser Arg Lys Leu Arg Ala Arg
180 50 55 60
182 Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
183 65 70 75 80

*Does Not Comply
Corrected Diskette Needed*

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185 Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
186 85 90 95
E--> 188 His Asn Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
E--> 189 100 105 110
191 Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala
E--> 192 115 120 125
194 His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His
E--> 195 130 135 140
197 Ser Phe Tyr Gly Pro Glu Pro Pro Val Pro Cys Gly Glu Leu Gly Ser
E--> 198 145 150 155 160
200 Pro Gly Gly Gly Ser Ser Gly Asp Trp Gly Ser Ile Tyr Ser Pro Val
E--> 201 165 170 175
203 Ser Gln Ala Gly Ser Leu Ser Pro Thr Ala Ser Leu Glu Glu Phe Pro
E--> 204 180 185 190
206 Gly Leu Gln Val Pro Ser Ser Pro Ser Cys Leu Leu Pro Gly Thr Leu
E--> 207 195 200 205
209 Val Phe Ser Asp Phe Leu
E--> 210 210
266 <210> SEQ ID NO: 10
267 <211> LENGTH: 214
268 <212> TYPE: PRT
269 <213> ORGANISM: Homo sapiens
271 <400> SEQUENCE: 10
272 Met Thr Pro Gln Pro Ser Gly Ala Pro Thr Val Gln Val Thr Arg Glu
273 1 5 10 15
275 Thr Glu Arg Ser Phe Pro Arg Ala Ser Glu Asp Glu Val Thr Cys Pro
276 20 25 30
278 Thr Ser Ala Pro Pro Ser Pro Thr Arg Thr Pro Gly Asn Cys Ala Glu
279 35 40 45
281 Ala Glu Glu Gly Gly Cys Arg Gly Ala Pro Arg Lys Leu Arg Ala Arg
282 50 55 60
284 Arg Gly Gly Arg Ser Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
285 65 70 75 80
287 Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
288 85 90 95
290 His Asp Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
291 100 105 110
293 Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala
294 115 120 125
296 His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His
297 130 135 140
E--> 299 Ser Leu Tyr Ala Leu Glu Pro Pro Ala Pro His Cys Gly Glu Leu Gly
300 145 150 155 160
302 Ser Pro Gly Gly Pro Pro Gly Asp Trp Gly Ser Leu Tyr Ser Pro Val
303 165 170 175
304 Ser Gln Ala Gly Ser Leu Ser Pro Ala Ala Ser Leu Glu Glu Arg Pro
305 180 185 190
307 Gly Leu Leu Gly Ala Thr Ser Ser Ala Cys Leu Ser Pro Gly Ser Leu
308 195 200 205

see p. 4
for explanation

OK - These
numbers are
in bold print
due to above
error

use "I", not "le"
numeral "1"
Glu

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310 Ala Phe Ser Asp Phe Leu
311 210

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<210> 8
<211> 214
<212> PRT
<213> Rattus norvegicus

<400> 8

Met Ala Pro His Pro Leu Asp Ala Pro Thr Ile Gln Val Ser Gln Glu
1 5 10 15
Thr Gln Gln Pro Phe Pro Gly Ala Ser Asp His Glu Val Leu Ser Ser
20 25 30
Asn Ser Thr Pro Pro Ser Pro Thr Leu Val Pro Arg Asp Cys Ser Glu
35 40 45
Ala Glu Ala Gly Asp Cys Arg Gly Thr Ser Arg Lys Leu Arg Ala Arg
50 55 60
Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
65 70 75 80
Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
85 90 95
His Asn Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
100 105 110

What does this mean? Is it a
typographical error? If it represents
a gap, then the amino acids following
it must be in a new sequence I.D. No.
and the <160> response must be
changed.

07/07/17

<210> 13

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 13

atcgttgaga ctcgtaccag cagagtcacg agagagacta cacggtactg gnnnnnnnnn 60

see p. 6 for error
explanation

VARIABLE LOCATION SUMMARY

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error explanation
Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:2; N Pos. 9,16

Seq#:13; N Pos. 52,53,54,55,56,57,58,59,60

See p. 7 for more error

VERIFICATION SUMMARY

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L:100 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:2
 L:100 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:2
 L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
 L:137 M:301 E: (44) No Sequence Data was Shown, SEQ ID:5
 L:137 M:252 E: No. of Seq. differs, <211> LENGTH:Input:18 Found:0 SEQ:5
 L:188 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:189 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
 M:332 Repeated in SeqNo=8
 L:210 M:252 E: No. of Seq. differs, <211> LENGTH:Input:214 Found:213 SEQ:8
 L:299 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
 L:347 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:13
 L:347 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:13
 L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
 L:499 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:501 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:26, <213>
 ORGANISM:Artificial Sequence
 L:501 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:501
 L:510 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:512 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>
 ORGANISM:Artificial Sequence
 L:512 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:512